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SEQUENCING LISTING

<110> KYOWA HAKKO KOGYO CO., LTD

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CARDIOMYOCYTES

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<151> 1999-12-28

<150> PCT-JP00-01148

<151> 2000-02-28

<150> PCT-JP00-07741

<151> 2000-11-02

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<170> PatentIn Ver.2.0

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 Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
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 Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
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 245 250 255
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Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly	
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Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
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 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
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 85 90 95
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 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
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Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu	
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Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp	
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cgc acc aac gcc aac ttc ctg gtg tgg ccg ccc tgt gtg gag gtg cag	384
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115 120 125	
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Arg	Asp	Gly	Lys	Pro	Cys	Leu	Gly	Asp	Ser	Ala	Pro	Tyr	Ala	Pro	Ala		
			225												240		
tac	ggc	gtg	ggc	ctc	aat	ccc	tac	ggt	tat	aac	gcc	tac	ccc	gcc	tat	768	
Tyr	Gly	Val	Gly	Leu	Asn	Pro	Tyr	Gly	Tyr	Asn	Ala	Tyr	Pro	Ala	Tyr		
				245											255		
ccg	ggt	tac	ggc	ggc	gcg	gcc	tgc	agc	cct	ggc	tac	agc	tgc	act	gcc	816	

Pro Gly Tyr Gly Gly Ala Ala Cys Ser Pro Gly Tyr Ser Cys Thr Ala
 260 265 270
 gct tac ccc gcc ggg cct tcc cca gcg cag ccg gcc act gcc gcc gcc 864
 Ala Tyr Pro Ala Gly Pro Ser Pro Ala Gln Pro Ala Thr Ala Ala Ala
 275 280 285
 aac aac aac ttc gtg aac ttc ggc gtc ggg gac ttg aat gcg gtt cag 912
 Asn Asn Asn Phe Val Asn Phe Gly Val Gly Asp Leu Asn Ala Val Gln
 290 295 300
 agc ccc ggg att ccg cag agc aac tcg gga gtg tcc acg ctg cat ggt 960
 Ser Pro Gly Ile Pro Gln Ser Asn Ser Gly Val Ser Thr Leu His Gly
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 atc cga gcc tgg 972
 ile Arg Ala Trp
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 Ala Ser Ser Pro Val Tyr Leu Pro Thr Pro Arg Val Pro Ser Ser Val
 35 40 45
 Leu Gly Leu Ser Tyr Leu Gln Gly Gly Gly Ala Gly Ser Ala Ser Gly
 50 55 60
 Gly Pro Ser Gly Gly Ser Pro Gly Gly Ala Ala Ser Gly Ala Gly Pro
 65 70 75 80
 Gly Thr Gln Gln Gly Ser Pro Gly Trp Ser Gln Ala Gly Ala Thr Gly
 85 90 95
 Ala Ala Tyr Thr Pro Pro Pro Val Ser Pro Arg Phe Ser Phe Pro Gly
 100 105 110
 Thr Thr Gly Ser Leu Ala Ala Ala Ala Ala Ala Ala Ala Arg Glu
 115 120 125
 Ala Ala Ala Tyr Ser Ser Gly Gly Gly Ala Ala Gly Ala Gly Leu Ala

130	135	140
Gly Arg Glu Gln Tyr	Gly Arg Ala Gly Phe Ala	Gly Ser Tyr Ser Ser
145	150	155
Pro Tyr Pro Ala Tyr	Met Ala Asp Val Gly Ala	Ser Trp Ala Ala Ala
165	170	175
Ala Ala Ala Ser Ala	Gly Pro Phe Asp Ser Pro	Val Leu His Ser Leu
180	185	190
Pro Gly Arg Ala Asn	Pro Ala Ala Arg His	Pro Asn Leu Asp Met Phe
195	200	205
Asp Asp Phe Ser Glu	Gly Arg Glu Cys Val Asn	Cys Gly Ala Met Ser
210	215	220
Thr Pro Leu Trp Arg	Arg Asp Gly Thr Gly	His Tyr Leu Cys Asn Ala
225	230	235
Cys Gly Leu Tyr His	Lys Met Asn Gly Ile	Asn Arg Pro Leu Ile Lys
245	250	255
Pro Gln Arg Arg Leu	Ser Ala Ser Arg Arg	Val Gly Leu Ser Cys Ala
260	265	270
Asn Cys Gln Thr Thr	Thr Thr Thr Leu Trp	Arg Arg Asn Ala Glu Gly
275	280	285
Glu Pro Val Cys Asn	Ala Cys Gly Leu Tyr	Met Lys Leu His Gly Val
290	295	300
Pro Arg Pro Leu Ala	Met Arg Lys Glu Gly	Ile Gln Thr Arg Lys Arg
305	310	315
Lys Pro Lys Asn Leu	Asn Lys Ser Lys Thr	Pro Ala Ala Pro Ser Gly
325	330	335
Ser Glu Ser Leu Pro	Pro Ala Ser Gly Ala	Ser Ser Asn Ser Ser Asn
340	345	350
Ala Thr Thr Ser Ser	Ser Glu Glu Met Arg	Pro Ile Lys Thr Glu Pro
355	360	365
Gly Leu Ser Ser His	Tyr Gly His Ser Ser	Ser Val Ser Gln Thr Phe
370	375	380
Ser Val Ser Ala Met	Ser Gly His Gly Pro	Ser Ile His Pro Val Leu
385	390	395
Ser Ala Leu Lys Leu	Ser Pro Gln Gly Tyr	Ala Ser Pro Val Ser Gln
405	410	415
Ser Pro Gln Thr Ser	Ser Lys Gln Asp Ser	Trp Asn Ser Leu Val Leu

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 Ala Asp Ser His Gly Asp Ile Ile Thr Ala
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 Ala Tyr Gln Ala Gly Gly Pro Gly Pro Phe Met His Gly Ala Gly Ala
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 gcg tcc tcg cca gtc tac ctg ccc aca ccg cgg gtg ccc tcc tcc gtt 144
 Ala Ser Ser Pro Val Tyr Leu Pro Thr Pro Arg Val Pro Ser Ser Val
 35 40 45
 ctg ggc ctg tcc tac ctc cag ggc gga ggc gcg ggc tct gcg tcc gga 192
 Leu Gly Leu Ser Tyr Leu Gln Gly Gly Gly Ala Gly Ser Ala Ser Gly
 50 55 60
 ggc ccc tcg ggc ggc agc ccc ggt ggg gcc gcg tct ggt gcg ggg ccc 240
 Gly Pro Ser Gly Gly Ser Pro Gly Gly Ala Ala Ser Gly Ala Gly Pro
 65 70 75 80
 ggg acc cag cag ggc agc ccg gga tgg agc cag gcg gga gcg acc gga 288
 Gly Thr Gln Gln Gly Ser Pro Gly Trp Ser Gln Ala Gly Ala Thr Gly
 85 90 95
 gcc gct tac acc ccg ccg ccg gtg tcg ccg cgc ttc tcc ttc ccg ggg 336
 Ala Ala Tyr Thr Pro Pro Pro Val Ser Pro Arg Phe Ser Phe Pro Gly
 100 105 110
 acc acc ggg tcc ctg gcg gcg gcg gcg gct gcc gcc gcc ccg gaa 384
 Thr Thr Gly Ser Leu Ala Ala Ala Ala Ala Ala Ala Ala Arg Glu
 115 120 125
 gct gcg gcc tac agc agt ggc ggc gga gcg gcg ggt gcg ggc ctg gcg 432

Ala Ala Ala Tyr Ser Ser Gly Gly Gly Ala Ala Gly Ala Gly Leu Ala	
130	135
ggc cgc gag cag tac ggg cgc gcc ggc ttc gcg ggc tcc tac tcc agc	480
Gly Arg Glu Gln Tyr Gly Arg Ala Gly Phe Ala Gly Ser Tyr Ser Ser	
145	150
ccc tac cgc gct tac atg gcc gac gtg ggc gcg tcc tgg gcc gca gcc	528
Pro Tyr Pro Ala Tyr Met Ala Asp Val Gly Ala Ser Trp Ala Ala Ala	
165	170
gcc gcc gcc tcc gcc ggc ccc ttc gac agc cgc gtc ctg cac agc ctg	576
Ala Ala Ala Ser Ala Gly Pro Phe Asp Ser Pro Val Leu His Ser Leu	
180	185
ccc ggc cgc gcc aac cgc gcc gcc cga cac ccc aat ctc gat atg ttt	624
Pro Gly Arg Ala Asn Pro Ala Ala Arg His Pro Asn Leu Asp Met Phe	
195	200
gac gac ttc tca gaa ggc aga gag tgt gtc aac tgt ggc gct atg tcc	672
Asp Asp Phe Ser Glu Gly Arg Glu Cys Val Asn Cys Gly Ala Met Ser	
210	215
acc cgc ctc tgg agg cga gat ggc acg ggt cac tat ctg tgc aac gcc	720
Thr Pro Leu Trp Arg Arg Asp Gly Thr Gly His Tyr Leu Cys Asn Ala	
225	230
tgt ggc ctc tac cac aag atg aac ggc atc aac cgc cgc ctc atc aag	768
Cys Gly Leu Tyr His Lys Met Asn Gly Ile Asn Arg Pro Leu Ile Lys	
245	250
cct cag cgc cgc ctg tcc gcc tcc cgc cga gtg ggc ctc tcc tgt gcc	816
Pro Gln Arg Arg Leu Ser Ala Ser Arg Arg Val Gly Leu Ser Cys Ala	
260	265
aac tgc cag acc acc acc acc acc acg ctg tgg cgc cgc aat ggc gag ggc	864
Asn Cys Gln Thr Thr Thr Thr Thr Leu Trp Arg Arg Asn Ala Glu Gly	
275	280
gag cct gtg tgc aat gcc tgc ggc ctc tac atg aag ctc cac ggc gtg	912
Glu Pro Val Cys Asn Ala Cys Gly Leu Tyr Met Lys Leu His Gly Val	
290	295
ccc agg cct ctt gca atg cgc aaa gag ggc atc caa acc aga aaa cgc	960
Pro Arg Pro Leu Ala Met Arg Lys Glu Gly Ile Gln Thr Arg Lys Arg	
305	310
aag ccc aag aac ctg aat aaa tct aag aca cca gca gct cct tca ggc	1008
	315
	320

Lys Pro Lys Asn Leu Asn Lys Ser Lys Thr Pro Ala Ala Pro Ser Gly
 325 330 335
 agt gag agc ctt cct ccc gcc agc ggt gct tcc agc aac tcc agc aac 1056
 Ser Glu Ser Leu Pro Pro Ala Ser Gly Ala Ser Ser Asn Ser Ser Asn
 340 345 350
 gcc acc acc agc agc agc gag gag atg cgt ccc atc aag acg gag cct 1104
 Ala Thr Thr Ser Ser Ser Glu Glu Met Arg Pro Ile Lys Thr Glu Pro
 355 360 365
 ggc ctg tca tct cac tac ggg cac agc agc tcc gtg tcc cag acg ttc 1152
 Gly Leu Ser Ser His Tyr Gly His Ser Ser Ser Val Ser Gln Thr Phe
 370 375 380
 tca gtc agt gcg atg tct ggc cat ggg ccc tcc atc cac cct gtc ctc 1200
 Ser Val Ser Ala Met Ser Gly His Gly Pro Ser Ile His Pro Val Leu
 385 390 395 400
 tcg gcc ctg aag ctc tcc cca caa ggc tat gcg tct ccc gtc agc cag 1248
 Ser Ala Leu Lys Leu Ser Pro Gln Gly Tyr Ala Ser Pro Val Ser Gln
 405 410 415
 tct cca cag acc agc tcc aag cag gac tct tgg aac agt ctg gtc ttg 1296
 Ser Pro Gln Thr Ser Ser Lys Gln Asp Ser Trp Asn Ser Leu Val Leu
 420 425 430
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 Ala Asp Ser His Gly Asp Ile Ile Thr Ala
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 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60

Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys
 85 90 95
 Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu
 100 105 110
 Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn
 115 120 125
 His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val
 130 135 140
 Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly
 145 150 155 160
 Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp
 165 170 175
 Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser
 180 185 190
 Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met
 195 200 205
 Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro
 210 215 220
 Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly
 225 230 235 240
 Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro
 245 250 255
 Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp
 260 265 270
 Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu
 275 280 285
 Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser
 290 295 300
 Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro
 305 310 315 320
 Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr
 325 330 335
 Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly
 340 345 350

Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln
 355 360 365
 Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly
 370 375 380
 Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile
 385 390 395 400
 Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro
 405 410 415
 Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro
 420 425 430
 Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln
 435 440 445
 Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser
 450 455 460
 Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro
 465 470 475 480
 Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser
 485 490 495
 Val Lys Arg Met Arg Met Asp Ala Trp Val Thr
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<210> 14

<211> 1521

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1524)

<400> 14

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1 5 10 15	
cga cag gtc act ttt aca aag aga aag ttt gga tta atg aag aaa gcc	96
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala	
20 25 30	
tat gaa ctt agt gtg ctc tgt gac tgt gaa ata gca ctc atc att ttc	144
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe	

35	40	45	
aac agc tct aac aaa ctg ttt caa tat gct agc act gat atg gac aaa			192
Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys			
50	55	60	
gtt ctt ctc aag tat aca gaa tat aat gaa cct cat gaa agc aga acc			240
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr			
65	70	75	80
aac tcg gat att gtt gag gct ctg aac aag aag gaa cac aga ggg tgc			288
Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys			
85	90	95	
gac agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa			336
Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu			
100	105	110	
gaa aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg cgg aat			384
Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn			
115	120	125	
cat aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc			432
His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val			
130	135	140	
aca gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg			480
Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly			
145	150	155	160
agt tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat			528
Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp			
165	170	175	
tca agc atg ctc tct cca cct caa acc aca tta cat aga aat gtg tct			576
Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser			
180	185	190	
cct gga gct cct cag aga cca cca agt act ggc aat gca ggt ggg atg			624
Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met			
195	200	205	
ttg agc act aca gac ctc aca gtg cca aat gga gct gga agc agt cca			672
Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro			
210	215	220	
gtg ggg aat gga ttt gta aac tca aga gct tct cca aat ttg att gga			720
Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly			

225	230	235	240	
gct act ggt gca aat agc tta ggc aaa gtc atg cct aca aag tct ccc	768			
Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro				
245	250	255		
cct cca cca ggt ggt ggt aat ctt gga atg aac agt agg aaa cca gat	816			
Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp				
260	265	270		
ctt cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta	864			
Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu				
275	280	285		
tcg gag gaa gag gaa ttg gag ttg aac acc caa agg atc agt agt tct	912			
Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser				
290	295	300		
caa gcc act caa cct ctt gct acc cca gtc gtg tct gtg aca acc cca	960			
Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro				
305	310	315	320	
agc ttg cct ccg caa gga ctt gtg tac tca gca atg ccg act gcc tac	1008			
Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr				
325	330	335		
aac act gat tat tca ctg acc agc gct gac ctg tca gcc ctt caa ggc	1056			
Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly				
340	345	350		
ttc aac tcg cca gga atg ctg tcg ctg gga cag gtg tcg gcc tgg cag	1104			
Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln				
355	360	365		
cag cac cac cta gga caa gca gcc ctc agc tct ctt gtt gct gga ggg	1152			
Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly				
370	375	380		
cag tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc	1200			
Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile				
385	390	395	400	
agc atc aag tcc gaa ccg att tca cct cct cgg gat cgt atg acc cca	1248			
Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro				
405	410	415		
tcg ggc ttc cag cag cag cag cag cag cag cag cag cag cag cag cag	1296			
Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro				

420	425	430	
cca cca ccg cag ccc cag cca caa ccc ccg cag ccc cag ccc cga cag			1344
Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln			
435	440	445	
gaa atg ggg cgc tcc cct gtg gac agt ctg agc agc tct agt agc tcc			1392
Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser			
450	455	460	
tat gat ggc agt gat cgg gag gat cca cgg ggc gac ttc cat tct cca			1440
Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro			
465	470	475	480
att gtg ctt ggc cga ccc cca aac act gag gac aga gaa agc cct tct			1488
Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser			
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gta aag cga atg agg atg gac gcg tgg gtg acc			1521
Val Lys Arg Met Arg Met Asp Ala Trp Val Thr			
500	505		
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Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala			
20 25 30			
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe			
35 40 45			
Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg			
50 55 60			
Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr			
65 70 75 80			
Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp			
85 90 95			
Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys			
100 105 110			
Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp Pro Ala Leu Pro Arg Pro			

115	120	125
Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr		
130	135	140
Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala		
145	150	155
Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys		
165	170	175
Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu		
180	185	190
Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg		
195	200	205
Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr		
210	215	220
Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr		
225	230	235
Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro		
245	250	255
Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro		
260	265	270
Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg		
275	280	285
Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys		
290	295	300
Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys		
305	310	315
Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly		
325	330	335
Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp		
340	345	350
Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys Thr Gln Gln		
355	360	

<210> 16

<211> 1095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1098)

<400> 16

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cgg cag gtg acg ttc acc aag cgg aag ttc ggg ctg atg aag aag gcc	96
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala	
20 25 30	
tat gag ctg agc gtg ctc tgt gac tgt gag ata gcc ctc atc atc ttc	144
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe	
35 40 45	
aac agc gcc aac cgc ctc ttc cag tat gcc agc acg gac atg gac cgt	192
Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg	
50 55 60	
gtg ctg ctg aag tac aca gag tac agc gag ccc cac gag agc cgc acc	240
Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr	
65 70 75 80	
aac act gac atc ctc gag acg ctg aag cgg agg ggc att ggc ctc gat	288
Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp	
85 90 95	
ggg cca gag ctg gag ccg gat gaa ggg cct gag gag cca gga gag aag	336
Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys	
100 105 110	
ttt cgg agg ctg gca ggc gaa ggg ggt gat ccg gcc ttg ccc cga ccc	384
Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp Pro Ala Leu Pro Arg Pro	
115 120 125	
cgg ctg tat cct gca gct cct gct atg ccc agc cca gat gtg gta tac	432
Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr	
130 135 140	
ggg gcc tta ccg cca cca ggc tgt gac ccc agt ggg ctt ggg gaa gca	480
Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala	
145 150 155 160	
ctg ccc gcc cag agc cgc cca tct ccc ttc cga cca gca gcc ccc aaa	528
Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys	
165 170 175	

gcc ggg ccc cca ggc ctg gtg cac cct ctc ttc tca cca agc cac ctc 576
 Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu
 180 185 190
 acc agc aag aca cca ccc cca ctg tac ctg ccg acg gaa ggg cgg agg 624
 Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg
 195 200 205
 tca gac ctg cct ggt ggc ctg gct ggg ccc cga ggg gga cta aac acc 672
 Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr
 210 215 220
 tcc aga agc ctc tac agt ggc ctg cag aac ccc tgc tcc act gca act 720
 Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr
 225 230 235 240
 ccc gga ccc cca ctg ggg agc ttc ccc ttc ctc ccc gga ggc ccc cca 768
 Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro
 245 250 255
 gtg ggg gcc gaa gcc tgg gcg agg agg gtc ccc caa ccc gcg gcg cct 816
 Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro
 260 265 270
 ccc cgc cga ccc ccc cag tca gca tca agt ctg agc gcc tct ctc cgg 864
 Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg
 275 280 285
 ccc ccg ggg gcc ccg gcg act ttc cta aga cct tcc cct atc cct tgc 912
 Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys
 290 295 300
 tcc tcg ccc ggt ccc tgg cag agc ctc tgc ggc ctg ggc ccg ccc tgc 960
 Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys
 305 310 315 320
 gcc ggc tgc cct tgg ccg acg gct ggc ccc ggt agg aga tca ccc ggt 1008
 Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly
 325 330 335
 ggc acc agc cca gag cgc tcg cca ggt acg gcg agg gca cgt ggg gac 1056
 Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp
 340 345 350
 ccc acc tcc ctc cag gcc tct tca gag aag acc caa cag 1095
 Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys Thr Gln Gln
 355 360 365

<210> 17

<211> 465

<212> PRT

<213> Homo sapiens

<400> 17

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 1 5 10 15
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Ser Asp Ile Val Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys
 85 90 95
 Asp Ser Pro Asp Pro Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu
 100 105 110
 Ser Glu Asp Lys Tyr Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile
 115 120 125
 Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro
 130 135 140
 Val Ser Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro
 145 150 155 160
 Val Ser Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser
 165 170 175
 Leu Gln Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser
 180 185 190
 Ala Gly Asn Thr Gly Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala
 195 200 205
 Gly Thr Ser Ala Gly Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly
 210 215 220
 Leu Leu Val Ser Pro Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser
 225 230 235 240
 Pro Pro Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg

	245		250		255										
Val	Leu	Ile	Pro	Pro	Gly	Ser	Lys	Asn	Thr	Met	Pro	Ser	Val	Asn	Gln
	260							265					270		
Arg	Ile	Asn	Asn	Ser	Gln	Ser	Ala	Gln	Ser	Leu	Ala	Thr	Pro	Val	Val
	275							280					285		
Ser	Val	Ala	Thr	Pro	Thr	Leu	Pro	Gly	Gln	Gly	Met	Gly	Gly	Tyr	Pro
	290							295					300		
Ser	Ala	Ile	Ser	Thr	Thr	Tyr	Gly	Thr	Glu	Tyr	Ser	Leu	Ser	Ser	Ala
305						310				315					320
Asp	Leu	Ser	Ser	Leu	Ser	Gly	Phe	Asn	Thr	Ala	Ser	Ala	Leu	His	Leu
				325					330					335	
Gly	Ser	Val	Thr	Gly	Trp	Gln	Gln	Gln	His	Leu	His	Asn	Met	Pro	Pro
			340					345						350	
Ser	Ala	Leu	Ser	Gln	Leu	Gly	Ala	Cys	Thr	Ser	Thr	His	Leu	Ser	Gln
	355						360					365			
Ser	Ser	Asn	Leu	Ser	Leu	Pro	Ser	Thr	Gln	Ser	Leu	Asn	Ile	Lys	Ser
	370					375						380			
Glu	Pro	Val	Ser	Pro	Pro	Arg	Asp	Arg	Thr	Thr	Thr	Pro	Ser	Arg	Tyr
385					390					395					400
Pro	Gln	His	Thr	Arg	His	Glu	Ala	Gly	Arg	Ser	Pro	Val	Asp	Ser	Leu
				405					410					415	
Ser	Ser	Cys	Ser	Ser	Ser	Tyr	Asp	Gly	Ser	Asp	Arg	Glu	Asp	His	Arg
		420						425					430		
Asn	Glu	Phe	His	Ser	Pro	Ile	Gly	Leu	Thr	Arg	Pro	Ser	Pro	Asp	Glu
	435						440					445			
Arg	Glu	Ser	Pro	Ser	Val	Lys	Arg	Met	Arg	Leu	Ser	Glu	Gly	Trp	Ala
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Thr

<210> 18

<211> 1395

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1398)

<400> 18

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aga cag gtg aca ttt aca aag agg aaa ttt ggg ttg atg aag aag gct	96
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala	
20 25 30	
tat gag ctg agc gtg ctg tgt gac tgt gag att gcg ctg atc atc ttc	144
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe	
35 40 45	
aac agc acc aac aag ctg ttc cag tat gcc agc acc gac atg gac aaa	192
Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys	
50 55 60	
gtg ctt ctc aag tac acg gag tac aac gag ccg cat gag agc cgg aca	240
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr	
65 70 75 80	
aac tca gac atc gtg gag acg ttg aga aag aag ggc ctt aat ggc tgt	288
Asn Ser Asp Ile Val Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys	
85 90 95	
gac agc cca gac ccc gat gcg gac gat tcc gta ggt cac agc cct gag	336
Asp Ser Pro Asp Pro Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu	
100 105 110	
tct gag gac aag tac agg aaa att aac gaa gat att gat cta atg atc	384
Ser Glu Asp Lys Tyr Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile	
115 120 125	
agc agg caa aga ttg tgt gct gtt cca cct ccc aac ttc gag atg cca	432
Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro	
130 135 140	
gtc tcc atc cca gtg tcc agc cac aac agt ttg gtg tac agc aac cct	480
Val Ser Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro	
145 150 155 160	
gtc agc tca ctg gga aac ccc aac cta ttg cca ctg get cac cct tct	528
Val Ser Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser	
165 170 175	
ctg cag agg aat agt atg tct cct ggt gta aca cat cga cct cca agt	576
Leu Gln Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser	
180 185 190	

gca ggt aac aca ggt ggt ctg atg ggt gga gac ctc acg tct ggt gca	624
Ala Gly Asn Thr Gly Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala	
195 200 205	
ggc acc agt gca ggg aac ggg tat ggc aat ccc cga aac tca cca ggt	672
Gly Thr Ser Ala Gly Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly	
210 215 220	
ctg ctg gtc tca cct ggt aac ttg aac aag aat atg caa gca aaa tct	720
Leu Leu Val Ser Pro Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser	
225 230 235 240	
cct ccc cca atg aat tta gga atg aat aac cgt aaa cca gat ctc cga	768
Pro Pro Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg	
245 250 255	
gtt ctt att cca cca ggc agc aag aat acg atg cca tca gtg aat caa	816
Val Leu Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Asn Gln	
260 265 270	
agg ata aat aac tcc cag tcg gct cag tca ttg gct acc cca gtg gtt	864
Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr Pro Val Val	
275 280 285	
tcc gta gca act cct act tta cca gga caa gga atg gga gga tat cca	912
Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly Gly Tyr Pro	
290 295 300	
tca gcc att tca aca aca tat ggt acc gag tac tct ctg agt agt gca	960
Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu Ser Ser Ala	
305 310 315 320	
gac ctg tca tct ctg tct ggg ttt aac acc gcc agc gct ctt cac ctt	1008
Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala Leu His Leu	
325 330 335	
ggt tca gta act ggc tgg caa cag caa cac cta cat aac atg cca cca	1056
Gly Ser Val Thr Gly Trp Gln Gln Gln His Leu His Asn Met Pro Pro	
340 345 350	
tct gcc ctc agt cag ttg gga gct tgc act agc act cat tta tct cag	1104
Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His Leu Ser Gln	
355 360 365	
agt tca aat ctc tcc ctg cct tet act caa agc ctc aac atc aag tca	1152
Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn Ile Lys Ser	
370 375 380	

gaa cct gtt tct cct cct aga gac cgt acc acc acc cct tcg aga tac 1200
 Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro Ser Arg Tyr
 385 390 395 400
 cca caa cac acg cgc cac gag gcg ggg aga tct cct gtt gac agc ttg 1248
 Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val Asp Ser Leu
 405 410 415
 agc agc tgt agc agt tcg tac gac ggg agc gac cga gag gat cac cgg 1296
 Ser Ser Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu Asp His Arg
 420 425 430
 aac gaa ttc cac tcc ccc att gga etc acc aga cct tcg ccg gac gaa 1344
 Asn Glu Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser Pro Asp Glu
 435 440 445
 agg gaa agt ccc tca gtc aag cgc atg cga ctt tct gaa gga tgg gca 1392
 Arg Glu Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu Gly Trp Ala
 450 455 460
 aca 1395
 Thr
 465
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 <211> 521
 <212> PRT
 <213> Homo sapiens
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 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys
 85 90 95
 Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu

	100		105		110
Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe					
115		120		125	
Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val					
130		135		140	
Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser					
145		150		155	160
Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser Leu Thr Asp Pro					
	165		170		175
Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg Asn Ser Val Ser					
	180		185		190
Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala Met Leu Gly Gly					
	195		200		205
Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro Val Gly Asn Gly					
	210		215		220
Tyr Val Ser Ala Arg Ala Ser Pro Gly Leu Leu Pro Val Ala Asn Gly					
225		230		235	240
Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro Pro Pro Pro Thr					
	245		250		255
His Ser Thr Gln Leu Gly Ala Pro Ser Arg Lys Pro Asp Leu Arg Val					
	260		265		270
Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His Leu Thr Glu Asp					
	275		280		285
His Leu Asp Leu Asn Asn Ala Gln Arg Leu Gly Val Ser Gln Ser Thr					
	290		295		300
His Ser Leu Thr Thr Pro Val Val Ser Val Ala Thr Pro Ser Leu Leu					
305		310		315	320
Ser Gln Gly Leu Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp					
	325		330		335
Tyr Gln Leu Thr Ser Ala Glu Leu Ser Ser Leu Pro Ala Phe Ser Ser					
	340		345		350
Pro Gly Gly Leu Ser Leu Gly Asn Val Thr Ala Trp Gln Gln Pro Gln					
	355		360		365
Gln Pro Gln Gln Pro Gln Gln Pro Gln Pro Pro Gln Gln Gln Pro Pro					
	370		375		380
Gln Pro Gln Gln Pro Gln Pro Gln Gln Pro Gln Gln Pro Gln Gln Pro					

385 390 395 400
 Pro Gln Gln Gln Ser His Leu Val Pro Val Ser Leu Ser Asn Leu Ile
 405 410 415
 Pro Gly Ser Pro Leu Pro His Val Gly Ala Ala Leu Thr Val Thr Thr
 420 425 430
 His Pro His Ile Ser Ile Lys Ser Glu Pro Val Ser Pro Ser Arg Glu
 435 440 445
 Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro Ala Ala Arg Pro
 450 455 460
 Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly Ser Tyr Glu Thr
 465 470 475 480
 Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro Thr Leu Gly Leu
 485 490 495
 Leu Arg Pro Ala Pro Glu Pro Glu Ala Glu Gly Ser Ala Val Lys Arg
 500 505 510
 Met Arg Leu Asp Thr Trp Thr Leu Lys
 515 520

<210> 20

<211> 1563

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1566)

<400> 20

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 1 5 10 15
 cga cag gtg act ttc acc aag cgg aag ttt ggc ctg atg aag aag gcg 96
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 tat gag ctg agc gtg cta tgt gac tgc gag atc gca ctc atc atc ttc 144
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 aac cac tcc aac aag ctg ttc cag tac gcc agc acc gac atg gac aag 192
 Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys

50	55	60	
gtg ctg ctc aag tac acg gag tac aat gag cca cac gag agc cgc acc			240
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr			
65	70	75	80
aac gcc gac atc atc gag acc ctg agg aag aag ggc ttc aat ggc tgc			288
Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys			
85	90	95	
gac agc ccc gag ccc gac ggg gag gac tcg ctg gaa cag agc ccc ctg			336
Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu			
100	105	110	
ctg gag gac aag tac cga cgc gcc agc gag gag ctc gac ggg ctc ttc			384
Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe			
115	120	125	
cgg cgc tat ggg tca act gtc ccg gcc ccc aac ttt gcc atg cct gtc			432
Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val			
130	135	140	
acg gtg ccc gtg tcc aat cag agc tca ctg cag ttc agc aat ccc agc			480
Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser			
145	150	155	160
ggc tcc ctg gtc acc cct tcc ctg gtg aca tca tcc ctc acg gac ccg			528
Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser Leu Thr Asp Pro			
165	170	175	
cgg ctc ctg tcc ccc cag cag cca gca cta cag agg aac agt gtg tct			576
Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg Asn Ser Val Ser			
180	185	190	
cct ggc ctg ccc cag cgg cca gct agt gcg ggg gcc atg ctg ggg ggt			624
Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala Met Leu Gly Gly			
195	200	205	
gac ctg aac agt gct aac gga gcc tgc ccc agc cct gtt ggg aat ggc			672
Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro Val Gly Asn Gly			
210	215	220	
tac gtc agt gct cgg gct tcc cct ggc ctc ctc cct gtg gcc aat ggc			720
Tyr Val Ser Ala Arg Ala Ser Pro Gly Leu Leu Pro Val Ala Asn Gly			
225	230	235	240
aac agc cta aac aag gtc atc cct gcc aag tct ccg ccc cca cct acc			768
Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro Pro Pro Pro Thr			

	245	250	255	
cac agc acc cag ctt gga gcc ccc	age cgc aag ccc gac ctg cga gtc	816		
His Ser Thr Gln Leu Gly Ala Pro	Ser Arg Lys Pro Asp Leu Arg Val			
260	265	270		
atc act tcc cag gca gga aag ggg tta atg cat cac ttg act gag gac	864			
Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His Leu Thr Glu Asp				
275	280	285		
cat tta gat ctg aac aat gcc cag cgc ctt ggg gtc tcc cag tct act	912			
His Leu Asp Leu Asn Asn Ala Gln Arg Leu Gly Val Ser Gln Ser Thr				
290	295	300		
cat tcg etc acc acc cca gtg gtt tct gtg gca acg ccg agt tta etc	960			
His Ser Leu Thr Thr Pro Val Val Ser Val Ala Thr Pro Ser Leu Leu				
305	310	315	320	
agc cag ggc etc ccc ttc tet tcc atg ccc act gcc tac aac aca gat	1008			
Ser Gln Gly Leu Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp				
325	330	335		
tac cag ttg acc agt gca gag etc tcc tcc tta cca gcc ttt agt tca	1056			
Tyr Gln Leu Thr Ser Ala Glu Leu Ser Ser Leu Pro Ala Phe Ser Ser				
340	345	350		
cct ggg ggg ctg tcg cta ggc aat gtc act gcc tgg caa cag cca cag	1104			
Pro Gly Gly Leu Ser Leu Gly Asn Val Thr Ala Trp Gln Gln Pro Gln				
355	360	365		
cag ccc cag cag ccg cag cag cca cag cct cca cag cag cag cca ccg	1152			
Gln Pro Gln Gln Pro Gln Gln Pro Gln Pro Pro Gln Gln Gln Pro Pro				
370	375	380		
cag cca cag cag cca cag cca cag cag cct cag cag ccg caa cag cca	1200			
Gln Pro Gln Gln Pro Gln Pro Gln Gln Pro Gln Gln Pro Gln Gln Pro				
385	390	395	400	
cct cag caa cag tcc cac ctg gtc cct gta tet etc agc aac etc atc	1248			
Pro Gln Gln Gln Ser His Leu Val Pro Val Ser Leu Ser Asn Leu Ile				
405	410	415		
ccg ggc agc ccc ctg ccc cac gtg ggt gct gcc etc aca gtc acc acc	1296			
Pro Gly Ser Pro Leu Pro His Val Gly Ala Ala Leu Thr Val Thr Thr				
420	425	430		
cac ccc cac atc agc atc aag tca gaa ccg gtg tcc cca agc cgt gag	1344			
His Pro His Ile Ser Ile Lys Ser Glu Pro Val Ser Pro Ser Arg Glu				

435	440	445	
cgc agc cct gcg cct ccc cct cca gct gtg ttc cca gct gcc cgc cct			1392
Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro Ala Ala Arg Pro			
450	455	460	
gag cct gcc gat ggt ctc agc agc cca gcc ggg gga tcc tat gag acg			1440
Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly Ser Tyr Glu Thr			
465	470	475	480
gga gac cgg gat gac gga cgg ggg gac ttc ggg ccc aca ctg gcc ctg			1488
Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro Thr Leu Gly Leu			
485	490	495	
ctg cgc cca gcc cca gag cct gag gct gag gcc tca gct gtg aag agg			1536
Leu Arg Pro Ala Pro Glu Pro Glu Ala Glu Gly Ser Ala Val Lys Arg			
500	505	510	
atg cgg ctt gat acc tgg aca tta aag			1563
Met Arg Leu Asp Thr Trp Thr Leu Lys			
515	520		

<210> 21

<211> 217

<212> PRT

<213> Rattus norvegicus

<400> 21

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20 25 30	
Ser Arg Cys Ser His Glu Glu Asn Pro Tyr Phe His Gly Trp Leu Ile	
35 40 45	
Gly His Pro Glu Met Ser Pro Pro Asp Tyr Ser Met Ala Leu Ser Tyr	
50 55 60	
Ser Pro Glu Tyr Ala Ser Gly Ala Ala Gly Leu Asp His Ser His Tyr	
65 70 75 80	
Gly Gly Val Pro Pro Gly Ala Gly Pro Pro Gly Leu Gly Gly Pro Arg	
85 90 95	
Pro Val Lys Arg Arg Gly Thr Ala Asn Arg Lys Glu Arg Arg Arg Thr	
100 105 110	
Gln Ser Ile Asn Ser Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn	

115	120	125
Val Pro Ala Asp Thr Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala		
130	135	140
Thr Ser Tyr Ile Ala Tyr Leu Met Asp Leu Leu Ala Lys Asp Asp Gln		
145	150	155
Asn Gly Glu Ala Glu Ala Phe Lys Ala Glu Ile Lys Lys Thr Asp Val		160
	165	170
Lys Glu Glu Lys Arg Lys Lys Glu Leu Asn Glu Ile Leu Lys Ser Thr		175
	180	185
Val Ser Ser Asn Asp Lys Lys Thr Lys Gly Arg Thr Gly Trp Pro Gln		190
	195	200
His Val Trp Ala Leu Glu Leu Lys Gln		205
210	215	

<210> 22

<211> 651

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<223> (1)..(654)

<400> 22

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Met Ser Leu Val Gly Gly Phe Pro His His Pro Val Val His His Glu	
1 5 10 15	
ggc tac ccg ttc gcc gca gcc gca gcc gcc gct gct gct gcc gcc gcc	96
Gly Tyr Pro Phe Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala	
20 25 30	
agc cgc tgc agt cac gag gag aac ccc tat ttc cac ggc tgg ctt att	144
Ser Arg Cys Ser His Glu Glu Asn Pro Tyr Phe His Gly Trp Leu Ile	
35 40 45	
ggc cac ccg gag atg tcg ccc ccc gac tac agc atg gcc ctg tcc tac	192
Gly His Pro Glu Met Ser Pro Pro Asp Tyr Ser Met Ala Leu Ser Tyr	
50 55 60	
agt ccc gag tac gcc agc ggt gcc ggc ggc ctg gac cac tcc cat tat	240
Ser Pro Glu Tyr Ala Ser Gly Ala Ala Gly Leu Asp His Ser His Tyr	
65 70 75 80	

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ggg gga gtg ccg ccc ggt gcc ggg cct ccc ggc ctg ggg ggg ccg cgc 288
Gly Gly Val Pro Pro Gly Ala Gly Pro Pro Gly Leu Gly Gly Pro Arg
      85                      90                      95

ccg gtg aag cgt cgg ggc acc gcc aac cgc aag gag cgg cgc agg act 336
Pro Val Lys Arg Arg Gly Thr Ala Asn Arg Lys Glu Arg Arg Arg Thr
      100                    105                    110

cag agc atc aac agc gcc ttc gcc gag ctg cgc gag tgc atc ccc aac 384
Gln Ser Ile Asn Ser Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn
      115                    120                    125

gtg ccc gcc gac acc aaa ctc tcc aaa atc aag act ctg cgc ctg gcc 432
Val Pro Ala Asp Thr Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala
      130                    135                    140

acc agc tac atc gcc tac ctc atg gat ctg ctg gcc aag gac gac cag 480
Thr Ser Tyr Ile Ala Tyr Leu Met Asp Leu Leu Ala Lys Asp Asp Gln
      145                    150                    155                    160

aac gga gag gcg gag gcc ttc aag gcg gag atc aag aag acc gac gtg 528
Asn Gly Glu Ala Glu Ala Phe Lys Ala Glu Ile Lys Lys Thr Asp Val
      165                    170                    175

aaa gag gag aag agg aag aaa gag ctg aat gaa atc ttg aaa agt aca 576
Lys Glu Glu Lys Arg Lys Lys Glu Leu Asn Glu Ile Leu Lys Ser Thr
      180                    185                    190

gtg agc agc aac gac aag aaa acc aaa ggc cgg aca ggc tgg cca cag 624
Val Ser Ser Asn Asp Lys Lys Thr Lys Gly Arg Thr Gly Trp Pro Gln
      195                    200                    205

cac gtc tgg gcc ctg gag ctc aag cag 651
His Val Trp Ala Leu Glu Leu Lys Gln
      210                    215

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<210> 23

<211> 215

<212> PRT

<213> Homo sapiens

<400> 23

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Met Asn Leu Val Gly Ser Tyr Ala His His His His His His Pro
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His Pro Ala His Pro Met Leu His Glu Pro Phe Leu Phe Gly Pro Ala
      20              25              30

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Ser Arg Cys His Gln Glu Arg Pro Tyr Phe Gln Ser Trp Leu Leu Ser
 35 40 45
 Pro Ala Asp Ala Ala Pro Asp Phe Pro Ala Gly Gly Pro Pro Pro Ala
 50 55 60
 Ala Ala Ala Ala Ala Thr Ala Tyr Gly Pro Asp Ala Arg Pro Gly Gln
 65 70 75 80
 Ser Pro Gly Arg Leu Glu Ala Leu Gly Gly Arg Leu Gly Arg Arg Lys
 85 90 95
 Gly Ser Gly Pro Lys Lys Glu Arg Arg Arg Thr Glu Ser Ile Asn Ser
 100 105 110
 Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn Val Pro Ala Asp Thr
 115 120 125
 Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala Thr Ser Tyr Ile Ala
 130 135 140
 Tyr Leu Met Asp Val Leu Ala Lys Asp Ala Gln Ser Gly Asp Pro Glu
 145 150 155 160
 Ala Phe Lys Ala Glu Leu Lys Lys Ala Asp Gly Gly Arg Glu Ser Lys
 165 170 175
 Arg Lys Arg Glu Leu Gln Gln His Glu Gly Phe Pro Pro Ala Leu Gly
 180 185 190
 Pro Val Glu Lys Arg Ile Lys Gly Arg Thr Gly Trp Pro Gln Gln Val
 195 200 205
 Trp Ala Leu Glu Leu Asn Gln
 210

<210> 24

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(648)

<400> 24

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 Met Asn Leu Val Gly Ser Tyr Ala His His His His His His His Pro
 1 5 10 15
 cac cct gcg cac ccc atg ctc cac gaa ccc ttc ctc ttc ggt ccg gcc 96

His Pro Ala	His Pro Met Leu	His Glu Pro Phe Leu Phe Gly Pro Ala	
20	25	30	
tgc cgc tgt cat cag gaa agg ccc tac ttc cag agc tgg ctg ctg agc	144		
Ser Arg Cys His Gln Glu Arg Pro Tyr Phe Gln Ser Trp Leu Leu Ser			
35	40	45	
ccg gct gac gct gcc ccg gac ttc cct gcg ggc ggg ccg ccg ccc gcg	192		
Pro Ala Asp Ala Ala Pro Asp Phe Pro Ala Gly Gly Pro Pro Pro Ala			
50	55	60	
gcc gct gca gcc gcc acc gcc tat ggt cct gac gcc agg cct ggg cag	240		
Ala Ala Ala Ala Ala Thr Ala Tyr Gly Pro Asp Ala Arg Pro Gly Gln			
65	70	75	80
agc ccc ggg cgg ctg gag gcg ctt ggc ggc cgt ctt ggc cgg cgg aaa	288		
Ser Pro Gly Arg Leu Glu Ala Leu Gly Gly Arg Leu Gly Arg Arg Lys			
85	90	95	
ggc tca gga ccc aag aag gag cgg aga cgc act gag agc att aac agc	336		
Gly Ser Gly Pro Lys Lys Glu Arg Arg Arg Thr Glu Ser Ile Asn Ser			
100	105	110	
gca ttc gcg gag ttg cgc gag tgc atc ccc aac gtg ccg gcc gac acc	384		
Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn Val Pro Ala Asp Thr			
115	120	125	
aag ctc tcc aag atc aag act ctg cgc cta gcc acc agc tac atc gcc	432		
Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala Thr Ser Tyr Ile Ala			
130	135	140	
tac ctg atg gac gtg ctg gcc aag gat gca cag tct ggc gat ccc gag	480		
Tyr Leu Met Asp Val Leu Ala Lys Asp Ala Gln Ser Gly Asp Pro Glu			
145	150	155	160
gcc ttc aag gct gaa ctc aag aag gcg gat ggc ggc cgt gag agc aag	528		
Ala Phe Lys Ala Glu Leu Lys Lys Ala Asp Gly Gly Arg Glu Ser Lys			
165	170	175	
cgg aaa agg gag ctg cag cag cac gaa ggt ttt cct cct gcc ctg ggc	576		
Arg Lys Arg Glu Leu Gln Gln His Glu Gly Phe Pro Pro Ala Leu Gly			
180	185	190	
cca gtc gag aag agg att aaa gga cgc acc ggc tgg ccg cag caa gtc	624		
Pro Val Glu Lys Arg Ile Lys Gly Arg Thr Gly Trp Pro Gln Gln Val			
195	200	205	
tgg gcg ctg gag tta aac cag	645		

Trp Ala Leu Glu Leu Asn Gln

210

215

<210> 25

<211> 411

<212> PRT

<213> Homo sapiens

<400> 25

Met	Glu	Arg	Met	Ser	Asp	Ser	Ala	Asp	Lys	Pro	Ile	Asp	Asn	Asp	Ala
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Glu	Gly	Val	Trp	Ser	Pro	Asp	Ile	Glu	Gln	Ser	Phe	Gln	Glu	Ala	Leu
			20					25					30		
Ala	Ile	Tyr	Pro	Pro	Cys	Gly	Arg	Arg	Lys	Ile	Ile	Leu	Ser	Asp	Glu
		35					40					45			
Gly	Lys	Met	Tyr	Gly	Arg	Asn	Glu	Leu	Ile	Ala	Arg	Tyr	Ile	Lys	Leu
	50					55				60					
Arg	Thr	Gly	Lys	Thr	Arg	Thr	Arg	Lys	Gln	Val	Ser	Ser	His	Ile	Gln
	65				70					75					80
Val	Leu	Ala	Arg	Arg	Lys	Ser	Arg	Asp	Phe	His	Ser	Lys	Leu	Lys	Asp
				85					90				95		
Gln	Thr	Ala	Lys	Asp	Lys	Ala	Leu	Gln	His	Met	Ala	Ala	Met	Ser	Ser
		100						105					110		
Ala	Gln	Ile	Val	Ser	Ala	Thr	Ala	Ile	His	Asn	Lys	Leu	Gly	Leu	Pro
		115					120						125		
Gly	Ile	Pro	Arg	Pro	Thr	Phe	Pro	Gly	Ala	Pro	Gly	Phe	Trp	Pro	Gly
	130					135					140				
Met	Ile	Gln	Thr	Gly	Gln	Pro	Gly	Ser	Ser	Gln	Asp	Val	Lys	Pro	Phe
	145				150					155				160	
Val	Gln	Gln	Ala	Tyr	Pro	Ile	Gln	Pro	Ala	Val	Thr	Ala	Pro	Ile	Pro
			165						170					175	
Gly	Phe	Glu	Pro	Ala	Ser	Ala	Pro	Ala	Pro	Ser	Val	Pro	Ala	Trp	Gln
		180						185					190		
Gly	Arg	Ser	Ile	Gly	Thr	Thr	Lys	Leu	Arg	Leu	Val	Glu	Phe	Ser	Ala
	195						200					205			
Phe	Leu	Glu	Gln	Gln	Arg	Asp	Pro	Asp	Ser	Tyr	Asn	Lys	His	Leu	Phe
	210					215					220				
Val	His	Ile	Gly	His	Ala	Asn	His	Ser	Tyr	Ser	Asp	Pro	Leu	Leu	Glu

225 230 235 240
 Ser Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly
 245 250 255
 Gly Leu Lys Glu Leu Phe Gly Lys Gly Pro Gln Asn Ala Phe Phe Leu
 260 265 270
 Val Lys Phe Trp Ala Asp Leu Asn Cys Asn Ile Gln Asp Asp Ala Gly
 275 280 285
 Ala Phe Tyr Gly Val Thr Ser Gln Tyr Glu Ser Ser Glu Asn Met Thr
 290 295 300
 Val Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu
 305 310 315 320
 Lys Val Glu Thr Glu Tyr Ala Arg Phe Glu Asn Gly Arg Phe Val Tyr
 325 330 335
 Arg Ile Asn Arg Ser Pro Met Cys Glu Tyr Met Ile Asn Phe Ile His
 340 345 350
 Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu
 355 360 365
 Asn Phe Thr Ile Leu Leu Val Val Thr Asn Arg Asp Thr Gln Glu Thr
 370 375 380
 Leu Leu Cys Met Ala Cys Val Phe Glu Val Ser Asn Ser Glu His Gly
 385 390 395 400
 Ala Gln His His Ile Tyr Arg Leu Val Lys Asp
 405 410

<210> 26

<211> 1233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1236)

<400> 26

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 Met Glu Arg Met Ser Asp Ser Ala Asp Lys Pro Ile Asp Asn Asp Ala
 1 5 10 15
 gaa ggg gtc tgg agc ccc gac atc gag caa agc ttt cag gag gcc ctg 96
 Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu

20	25	30	
get atc tat cca cca tgt ggg agg agg aaa atc atc tta tca gac gaa	144		
Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu			
35	40	45	
ggc aaa atg tat ggt agg aat gaa ttg ata gcc aga tac atc aaa ctc	192		
Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu			
50	55	60	
agg aca ggc aag acg agg acc aga aaa cag gtg tct agt cac att cag	240		
Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln			
65	70	75	80
gtt ctt gcc aga agg aaa tct cgt gat ttt cat tcc aag cta aag gat	288		
Val Leu Ala Arg Arg Lys Ser Arg Asp Phe His Ser Lys Leu Lys Asp			
85	90	95	
cag act gca aag gat aag gcc ctg cag cac atg gcg gcc atg tcc tca	336		
Gln Thr Ala Lys Asp Lys Ala Leu Gln His Met Ala Ala Met Ser Ser			
100	105	110	
gcc cag atc gtc tcg gcc act gcc att cat aac aag ctg ggg ctg cct	384		
Ala Gln Ile Val Ser Ala Thr Ala Ile His Asn Lys Leu Gly Leu Pro			
115	120	125	
ggg att cca cgc ccg acc ttc cca ggg gcg ccg ggg ttc tgg ccg gga	432		
Gly Ile Pro Arg Pro Thr Phe Pro Gly Ala Pro Gly Phe Trp Pro Gly			
130	135	140	
atg att caa aca ggg cag cca gga tcc tca caa gac gtc aag cct ttt	480		
Met Ile Gln Thr Gly Gln Pro Gly Ser Ser Gln Asp Val Lys Pro Phe			
145	150	155	160
gtg cag cag gcc tac ccc atc cag cca gcg gtc aca gcc ccc att cca	528		
Val Gln Gln Ala Tyr Pro Ile Gln Pro Ala Val Thr Ala Pro Ile Pro			
165	170	175	
ggg ttt gag cct gca tog gcc cca gct ccc tca gtc cct gcc tgg caa	576		
Gly Phe Glu Pro Ala Ser Ala Pro Ala Pro Ser Val Pro Ala Trp Gln			
180	185	190	
ggt cgc tcc att ggc aca acc aag ctt cgc ctg gtg gaa ttt tca get	624		
Gly Arg Ser Ile Gly Thr Thr Lys Leu Arg Leu Val Glu Phe Ser Ala			
195	200	205	
ttt ctc gag cag cag cga gac cca gac tcg tac aac aaa cac ctc ttc	672		
Phe Leu Glu Gln Gln Arg Asp Pro Asp Ser Tyr Asn Lys His Leu Phe			

210	215	220	
gtg cac att ggg cat gcc aac cat tct tac agt gac cca ttg ctt gaa			720
Val His Ile Gly His Ala Asn His Ser Tyr Ser Asp Pro Leu Leu Glu			
225	230	235	240
tca gtg gac att cgt cag att tat gac aaa ttt cct gaa aag aaa ggt			768
Ser Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly			
	245	250	255
ggc tta aag gaa ctg ttt gga aag ggc cct caa aat gcc ttc ttc ctc			816
Gly Leu Lys Glu Leu Phe Gly Lys Gly Pro Gln Asn Ala Phe Phe Leu			
	260	265	270
gta aaa ttc tgg gct gat tta aac tgc aat att caa gat gat gct ggg			864
Val Lys Phe Trp Ala Asp Leu Asn Cys Asn Ile Gln Asp Asp Ala Gly			
	275	280	285
gct ttt tat ggt gta acc agt cag tac gag agt tct gaa aat atg aca			912
Ala Phe Tyr Gly Val Thr Ser Gln Tyr Glu Ser Ser Glu Asn Met Thr			
	290	295	300
gtc acc tgt tcc acc aaa gtt tgc tcc ttt ggg aag caa gta gta gaa			960
Val Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu			
	305	310	315
aaa gta gag acg gag tat gca agg ttt gag aat ggc cga ttt gta tac			1008
Lys Val Glu Thr Glu Tyr Ala Arg Phe Glu Asn Gly Arg Phe Val Tyr			
	325	330	335
cga ata aac cgc tcc cca atg tgt gaa tat atg atc aac ttc atc cac			1056
Arg Ile Asn Arg Ser Pro Met Cys Glu Tyr Met Ile Asn Phe Ile His			
	340	345	350
aag ctc aaa cac tta cca gag aaa tat atg atg aac agt gtt ttg gaa			1104
Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu			
	355	360	365
aac ttc aca att tta ttg gtg gta aca aac agg gat aca caa gaa act			1152
Asn Phe Thr Ile Leu Leu Val Val Thr Asn Arg Asp Thr Gln Glu Thr			
	370	375	380
cta ctc tgc atg gcc tgt gtg ttt gaa gtt tca aat agt gaa cac gga			1200
Leu Leu Cys Met Ala Cys Val Phe Glu Val Ser Asn Ser Glu His Gly			
	385	390	395
gca caa cat cat att tac agg ctt gta aag gac			1233
Ala Gln His His Ile Tyr Arg Leu Val Lys Asp			

405

410

<210> 27

<211> 427

<212> PRT

<213> Homo sapiens

<400> 27

Ile	Thr	Ser	Asn	Glu	Trp	Ser	Ser	Pro	Thr	Ser	Pro	Glu	Gly	Ser	Thr
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Ala	Ser	Gly	Gly	Ser	Gln	Ala	Leu	Asp	Lys	Pro	Ile	Asp	Asn	Asp	Ala
			20					25					30		
Glu	Gly	Val	Trp	Ser	Pro	Asp	Ile	Glu	Gln	Ser	Phe	Gln	Glu	Ala	Leu
		35					40					45			
Ala	Ile	Tyr	Pro	Pro	Cys	Gly	Arg	Arg	Lys	Ile	Ile	Leu	Ser	Asp	Glu
	50					55					60				
Gly	Lys	Met	Tyr	Gly	Arg	Asn	Glu	Leu	Ile	Ala	Arg	Tyr	Ile	Lys	Leu
65					70				75					80	
Arg	Thr	Gly	Lys	Thr	Arg	Thr	Arg	Lys	Gln	Val	Ser	Ser	His	Ile	Gln
			85						90					95	
Val	Leu	Ala	Arg	Arg	Lys	Ala	Arg	Glu	Ile	Gln	Ala	Lys	Leu	Lys	Asp
			100					105					110		
Gln	Ala	Ala	Lys	Asp	Lys	Ala	Leu	Gln	Ser	Met	Ala	Ala	Met	Ser	Ser
		115					120					125			
Ala	Gln	Ile	Ile	Ser	Ala	Thr	Ala	Phe	His	Ser	Ser	Met	Ala	Leu	Ala
	130					135						140			
Arg	Gly	Pro	Gly	Arg	Pro	Ala	Val	Ser	Gly	Phe	Trp	Gln	Gly	Ala	Leu
145					150				155					160	
Pro	Gly	Gln	Ala	Gly	Thr	Ser	His	Asp	Val	Lys	Pro	Phe	Ser	Gln	Gln
			165					170					175		
Thr	Tyr	Ala	Val	Gln	Pro	Pro	Leu	Pro	Leu	Pro	Gly	Phe	Glu	Ser	Pro
		180					185						190		
Ala	Gly	Pro	Ala	Pro	Ser	Pro	Ser	Ala	Pro	Pro	Ala	Pro	Pro	Trp	Gln
		195					200					205			
Gly	Arg	Ser	Val	Ala	Ser	Ser	Lys	Leu	Trp	Met	Leu	Glu	Phe	Ser	Ala
	210					215				220					
Phe	Leu	Glu	Gln	Gln	Gln	Asp	Pro	Asp	Thr	Tyr	Asn	Lys	His	Leu	Phe
225					230					235				240	

Val His Ile Gly Gln Ser Ser Pro Ser Tyr Ser Asp Pro Tyr Leu Glu
 245 250 255
 Ala Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly
 260 265 270
 Gly Leu Lys Asp Leu Phe Glu Arg Gly Pro Ser Asn Ala Phe Phe Leu
 275 280 285
 Val Lys Phe Trp Ala Asp Leu Asn Thr Asn Ile Glu Asp Glu Gly Ser
 290 295 300
 Ser Phe Tyr Gly Val Ser Ser Gln Tyr Glu Ser Pro Glu Asn Met Ile
 305 310 315 320
 Ile Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu
 325 330 335
 Lys Val Glu Thr Glu Tyr Ala Arg Tyr Glu Asn Gly His Tyr Ser Tyr
 340 345 350
 Arg Ile His Arg Ser Pro Leu Cys Glu Tyr Met Ile Asn Phe Ile His
 355 360 365
 Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu
 370 375 380
 Asn Phe Thr Ile Leu Gln Val Val Thr Asn Arg Asp Thr Gln Glu Thr
 385 390 395 400
 Leu Leu Cys Ile Ala Tyr Val Phe Glu Val Ser Ala Ser Glu His Gly
 405 410 415
 Ala Gln His His Ile Tyr Arg Leu Val Lys Glu
 420 425

<210> 28

<211> 1281

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1284)

<400> 28

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 gcc tct ggg ggc agt cag gca ctg gac aag ccc atc gac aat gac gca 96

Ala Ser Gly Gly Ser Gln Ala Leu Asp Lys Pro Ile Asp Asn Asp Ala	
20 25 30	
gag ggc gtg tgg agc cgc gat att gag cag agt ttc cag gag gcc ctc	144
Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu	
35 40 45	
gcc atc tac cgc ccc tgt ggc agg cgc aaa atc atc ctg tcg gac gag	192
Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu	
50 55 60	
ggc aag atg tat ggt cgg aac gag ctg att gcc cgc tac atc aag ctc	240
Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu	
65 70 75 80	
cgg aca ggg aag acc cgc acc agg aag cag gtc tcc agc cac atc cag	288
Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln	
85 90 95	
gtg ctg gct cgt cgc aaa gct cgc gag atc cag gcc aag cta aag gac	336
Val Leu Ala Arg Arg Lys Ala Arg Glu Ile Gln Ala Lys Leu Lys Asp	
100 105 110	
cag gca gct aag gac aag gcc ctg cag agc atg gct gcc atg tcg tct	384
Gln Ala Ala Lys Asp Lys Ala Leu Gln Ser Met Ala Ala Met Ser Ser	
115 120 125	
gca cag atc atc tcc gcc acg gcc ttc cac agt agc atg gcc ctc gcc	432
Ala Gln Ile Ile Ser Ala Thr Ala Phe His Ser Ser Met Ala Leu Ala	
130 135 140	
cgg ggc ccc ggc cgc cca gca gtc tca ggg ttt tgg caa gga gct ttg	480
Arg Gly Pro Gly Arg Pro Ala Val Ser Gly Phe Trp Gln Gly Ala Leu	
145 150 155 160	
cca ggc caa gcc gga acg tcc cat gat gtg aag cct ttc tct cag caa	528
Pro Gly Gln Ala Gly Thr Ser His Asp Val Lys Pro Phe Ser Gln Gln	
165 170 175	
acc tat gct gtc cag cct cgc ctg cct ctg cca ggg ttt gag tct cct	576
Thr Tyr Ala Val Gln Pro Pro Leu Pro Leu Pro Gly Phe Glu Ser Pro	
180 185 190	
gca ggg ccc gcc cca tcg ccc tct gcg ccc ccg gca ccc cca tgg cag	624
Ala Gly Pro Ala Pro Ser Pro Ser Ala Pro Pro Ala Pro Pro Trp Gln	
195 200 205	
ggc cgc agc gtg gcc agc tcc aag ctc tgg atg ttg gag ttc tct gcc	672

Gly Arg Ser Val Ala Ser Ser Lys Leu Trp Met Leu Glu Phe Ser Ala	
210	215 220
ttc ctg gag cag cag cag gac ccg gac acg tac aac aag cac ctg ttc	720
Phe Leu Glu Gln Gln Gln Asp Pro Asp Thr Tyr Asn Lys His Leu Phe	
225	230 235 240
gtg cac att ggc cag tcc agc cca agc tac agc gac ccc tac ctc gaa	768
Val His Ile Gly Gln Ser Ser Pro Ser Tyr Ser Asp Pro Tyr Leu Glu	
245	250 255
gcc gtg gac atc cgc caa atc tat gac aaa ttc ccg gag aaa aag ggt	816
Ala Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly	
260	265 270
gga ctc aag gat ctc ttc gaa cgg gga ccc tcc aat gcc ttt ttt ctt	864
Gly Leu Lys Asp Leu Phe Glu Arg Gly Pro Ser Asn Ala Phe Phe Leu	
275	280 285
gtg aag ttc tgg gca gac ctc aac acc aac atc gag gat gaa ggc agc	912
Val Lys Phe Trp Ala Asp Leu Asn Thr Asn Ile Glu Asp Glu Gly Ser	
290	295 300
tcc ttc tat ggg gtc tcc agc cag tat gag agc ccc gag aac atg atc	960
Ser Phe Tyr Gly Val Ser Ser Gln Tyr Glu Ser Pro Glu Asn Met Ile	
305	310 315 320
atc acc tgc tcc acg aag gtc tgc tct ttc ggc aag cag gtg gtg gag	1008
Ile Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu	
325	330 335
aaa gtt gag aca gag tat gct cgc tat gag aat gga cac tac tct tac	1056
Lys Val Glu Thr Glu Tyr Ala Arg Tyr Glu Asn Gly His Tyr Ser Tyr	
340	345 350
cgc atc cac cgg tcc ccg ctc tgt gag tac atg atc aac ttc atc cac	1104
Arg Ile His Arg Ser Pro Leu Cys Glu Tyr Met Ile Asn Phe Ile His	
355	360 365
aag ctc aag cac ctc cct gag aag tac atg atg aac agc gtg ctg gag	1152
Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu	
370	375 380
aac ttc acc atc ctg cag gtg gtc acc aac aga gac aca cag gag acc	1200
Asn Phe Thr Ile Leu Gln Val Val Thr Asn Arg Asp Thr Gln Glu Thr	
385	390 395 400
ttg ctg tgc att gcc tat gtc ttt gag gtg tca gcc agt gag cac ggg	1248

Leu Leu Cys Ile Ala Tyr Val Phe Glu Val Ser Ala Ser Glu His Gly
 405 410 415
 gct cag cac cac atc tac agg ctg gtg aaa gaa 1281
 Ala Gln His His Ile Tyr Arg Leu Val Lys Glu
 420 425
 <210> 29
 <211> 435
 <212> PRT
 <213> Homo sapiens
 <400> 29
 Ile Ala Ser Asn Ser Trp Asn Ala Ser Ser Ser Pro Gly Glu Ala Arg
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 Glu Asp Gly Pro Glu Gly Leu Asp Lys Gly Leu Asp Asn Asp Ala Glu
 20 25 30
 Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu Ala
 35 40 45
 Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu Gly
 50 55 60
 Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu Arg
 65 70 75 80
 Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln Val
 85 90 95
 Leu Ala Arg Lys Lys Val Arg Glu Tyr Gln Val Gly Ile Lys Ala Met
 100 105 110
 Asn Leu Asp Gln Val Ser Lys Asp Lys Ala Leu Gln Ser Met Ala Ser
 115 120 125
 Met Ser Ser Ala Gln Ile Val Ser Ala Ser Val Leu Gln Asn Lys Phe
 130 135 140
 Ser Pro Pro Ser Pro Leu Pro Gln Ala Val Phe Ser Thr Ser Ser Arg
 145 150 155 160
 Phe Trp Ser Ser Pro Pro Leu Leu Gly Gln Gln Pro Gly Pro Ser Gln
 165 170 175
 Asp Ile Lys Pro Phe Ala Gln Pro Ala Tyr Pro Ile Gln Pro Pro Leu
 180 185 190
 Pro Pro Thr Leu Ser Ser Tyr Glu Pro Leu Ala Pro Leu Pro Ser Ala
 195 200 205

Ala Ala Ser Val Pro Val Trp Gln Asp Arg Thr Ile Ala Ser Ser Arg
 210 215 220
 Leu Arg Leu Leu Glu Tyr Ser Ala Phe Met Glu Val Gln Arg Asp Pro
 225 230 235 240
 Asp Thr Tyr Ser Lys His Leu Phe Val His Ile Gly Gln Thr Asn Pro
 245 250 255
 Ala Phe Ser Asp Pro Pro Leu Glu Ala Val Asp Val Arg Gln Ile Tyr
 260 265 270
 Asp Lys Phe Pro Glu Lys Lys Gly Gly Leu Lys Glu Leu Tyr Glu Lys
 275 280 285
 Gly Pro Pro Asn Ala Phe Phe Leu Val Lys Phe Trp Ala Asp Leu Asn
 290 295 300
 Ser Thr Ile Gln Glu Gly Pro Gly Ala Phe Tyr Gly Val Ser Ser Gln
 305 310 315 320
 Tyr Ser Ser Ala Asp Ser Met Thr Ile Ser Val Ser Thr Lys Val Cys
 325 330 335
 Ser Phe Gly Lys Gln Val Val Glu Lys Val Glu Thr Glu Tyr Ala Arg
 340 345 350
 Leu Glu Asn Gly Arg Phe Val Tyr Arg Ile His Arg Ser Pro Met Cys
 355 360 365
 Glu Tyr Met Ile Asn Phe Ile His Lys Leu Lys His Leu Pro Glu Lys
 370 375 380
 Tyr Met Met Asn Ser Val Leu Glu Asn Phe Thr Ile Leu Gln Val Val
 385 390 395 400
 Thr Ser Arg Asp Ser Gln Glu Thr Leu Leu Val Ile Ala Phe Val Phe
 405 410 415
 Glu Val Ser Thr Ser Glu His Gly Ala Gln His His Val Tyr Lys Leu
 420 425 430

Val Lys Asp

<210> 30

<211> 1305

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1305)

<400> 30

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gag gat ggg ccc gag ggc ctg gac aag ggg ctg gac aac gat gcg gag	96
Glu Asp Gly Pro Glu Gly Leu Asp Lys Gly Leu Asp Asn Asp Ala Glu	
20 25 30	
ggc gtg tgg agc ccg gac atc gag cag agc ttc cag gag gcc ctg gcc	144
Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu Ala	
35 40 45	
atc tac ccg ccc tgc ggc cgg cgg aag atc atc ctg tca gac gag ggc	192
Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu Gly	
50 55 60	
aag atg tac ggc cga aat gag ttg att gca cgc tat att aaa ctg agg	240
Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu Arg	
65 70 75 80	
acg ggg aag act cgg acg aga aaa cag gtg tcc agc cac ata cag gtt	288
Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln Val	
85 90 95	
cta gct cgg aag aag gtg cgg gag tac cag gtt ggc atc aag gcc atg	336
Leu Ala Arg Lys Lys Val Arg Glu Tyr Gln Val Gly Ile Lys Ala Met	
100 105 110	
aac ctg gac cag gtc tcc aag gac aaa gcc ctt cag agc atg gcg tcc	384
Asn Leu Asp Gln Val Ser Lys Asp Lys Ala Leu Gln Ser Met Ala Ser	
115 120 125	
atg tcc tct gcc cag atc gtc tct gcc agt gtc ctg cag aac aag ttc	432
Met Ser Ser Ala Gln Ile Val Ser Ala Ser Val Leu Gln Asn Lys Phe	
130 135 140	
agc cca cct tcc cct ctg ccc cag gcc gtc ttc tcc act tcc tcg cgg	480
Ser Pro Pro Ser Pro Leu Pro Gln Ala Val Phe Ser Thr Ser Ser Arg	
145 150 155 160	
ttc tgg agc agc ccc cct ctc ctg gga cag cag cct gga ccc tct cag	528
Phe Trp Ser Ser Pro Pro Leu Leu Gly Gln Gln Pro Gly Pro Ser Gln	
165 170 175	
gac atc aag ccc ttt gca cag cea gcc tac ccc atc cag ccg ccc ctg	576
Asp Ile Lys Pro Phe Ala Gln Pro Ala Tyr Pro Ile Gln Pro Pro Leu	

180	185	190	
ccg ccg acg ctc agc agt tat gag ccc ctg gcc ccg ctc ccc tca gct	624		
Pro Pro Thr Leu Ser Ser Tyr Glu Pro Leu Ala Pro Leu Pro Ser Ala			
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gct gcc tct gtg cct gtg tgg cag gac cgt acc att gcc tcc tcc cgg	672		
Ala Ala Ser Val Pro Val Trp Gln Asp Arg Thr Ile Ala Ser Ser Arg			
210	215	220	
ctg cgg ctc ctg gag tat tca gcc ttc atg gag gtg cag cga gac cct	720		
Leu Arg Leu Leu Glu Tyr Ser Ala Phe Met Glu Val Gln Arg Asp Pro			
225	230	235	240
gac acg tac agc aaa cac ctg ttt gtg cac atc gcc cag acg aac ccc	768		
Asp Thr Tyr Ser Lys His Leu Phe Val His Ile Gly Gln Thr Asn Pro			
245	250	255	
gcc ttc tca gac cca ccc ctg gag gca gta gat gtg cgc cag atc tat	816		
Ala Phe Ser Asp Pro Pro Leu Glu Ala Val Asp Val Arg Gln Ile Tyr			
260	265	270	
gac aaa ttc ccc gag aaa aag gga gga ttg aag gag ctc tat gag aag	864		
Asp Lys Phe Pro Glu Lys Lys Gly Gly Leu Lys Glu Leu Tyr Glu Lys			
275	280	285	
ggg ccc cct aat gcc ttc ttc ctt gtc aag ttc tgg gcc gac ctc aac	912		
Gly Pro Pro Asn Ala Phe Phe Leu Val Lys Phe Trp Ala Asp Leu Asn			
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agc acc atc cag gag ggc ccg gga gcc ttc tat ggg gtc agc tct cag	960		
Ser Thr Ile Gln Glu Gly Pro Gly Ala Phe Tyr Gly Val Ser Ser Gln			
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tac agc tct gct gat agc atg acc atc agc gtc tcc acc aag gtg tgc	1008		
Tyr Ser Ser Ala Asp Ser Met Thr Ile Ser Val Ser Thr Lys Val Cys			
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tcc ttt ggc aaa cag gtg gta gag aag gtg gag act gag tat gcc agg	1056		
Ser Phe Gly Lys Gln Val Val Glu Lys Val Glu Thr Glu Tyr Ala Arg			
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ctg gag aac ggg cgc ttt gtg tac cgt atc cac cgc tgc ccc atg tgc	1104		
Leu Glu Asn Gly Arg Phe Val Tyr Arg Ile His Arg Ser Pro Met Cys			
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gag tac atg atc aac ttc atc cac aag ctg aag cac ctg ccc gag aag	1152		
Glu Tyr Met Ile Asn Phe Ile His Lys Leu Lys His Leu Pro Glu Lys			

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tac atg atg aac agc gtg ctg gag aac ttc acc atc ctg cag gtg gtc			1200
Tyr Met Met Asn Ser Val Leu Glu Asn Phe Thr Ile Leu Gln Val Val			
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Thr Ser Arg Asp Ser Gln Glu Thr Leu Leu Val Ile Ala Phe Val Phe			
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gaa gtc tcc acc agt gag cac ggg gcc cag cac cat gtc tac aag ctc			1296
Glu Val Ser Thr Ser Glu His Gly Ala Gln His His Val Tyr Lys Leu			
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Val Lys Asp			
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Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr			
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Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val			
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Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
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 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
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 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
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 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
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 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
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 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
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 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
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 465 470 475 480
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 485 490 495
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 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
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 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
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 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
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 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
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 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
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 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
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 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
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 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
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 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
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 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
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 995 1000 1005

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 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
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 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
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Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
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gag gcc ttc acc acc agc gtg cgc agc tac ctg ccc aac acg gtg acc 384
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
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Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
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Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175
cag ctc ggc gct gcc act cag gcc cgg ccc ccg cca cac gct agt gga 576
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190
ccc cga agg cgt ctg gga tgc gaa cgg gcc tgg aac cat agc gtc agg 624
Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205
gag gcc ggg gtc ccc ctg ggc ctg cca gcc ccg ggt gcg agg agg cgc 672
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245 250 255

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gcc cac ccg ggc agg acg cgt gga ccg agt gac cgt ggt ttc tgt gtg 816
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 gtg tca cct gcc aga ccc gcc gaa gaa gcc acc tct ttg gag ggt gcg 864
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
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 ctc tct ggc acg cgc cac tcc cac cca tcc gtg ggc cgc cag cac cac 912
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 290 295 300
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 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 gcg cag tgc ccc tac ggg gtg ctc ctc aag acg cac tgc ccg ctg cga 1248
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 gct gcg gtc acc cca gca gcc ggt gtc tgt gcc cgg gag aag ccc cag 1296
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
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Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser	
465 470 475 480	
agg cac aac gaa cgc cgc ttc ctc agg aac acc aag aag ttc atc tcc	1488
Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser	
485 490 495	
ctg ggg aag cat gcc aag ctc tgc ctg cag gag ctg acg tgg aag atg	1536
Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met	
500 505 510	
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Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys	
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Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe	
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Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg	
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Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala	
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Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys	
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                1045                1050                1055
ggg gcc aag ggc gcc gcc ggc cct ctg ccc tcc gag gcc gtg cag tgg 3216
Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
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ctg tgc cac caa gca ttc ctg ctc aag ctg act cga cac cgt gtc acc 3264
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Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
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1105                1110                1115                1120
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<210> 39

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<400> 40

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24

<210> 41

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 41

ctctctctcc tcaggacaa

19

<210> 42

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 42

tggagcaaaa cagaatggct gg 22

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 43

ctgagatgtc tctctctctc ttag 24

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 44

acaatgactg atgagagatg 20

<210> 45

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 45

cagacctgaa ggagacct 18

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 46

gtcagcgtaa acagttgc

18

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 47

gccaaagaagc ggatagaagg

20

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 48

ctgtggttca gggctcagtc

20

<210> 49

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 49

cagtggagct ggacaaagcc

20

<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 50

tagcgacggt tctggaacca 20

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 51

ctgtcatctc actatgggca 20

<210> 52

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 52

ccaagtccga gcaggaattt 20

<210> 53

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 53

aagacgtcaa gccctttgtg 20

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 54

aaaggagcac actttggtgg

20

<210> 55

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 55

agcaagaata cgatgccatc

20

<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223>Description of Artificial Sequence: artificially synthesized primer sequence

<400> 56

gaaggggtgg tggtagcggtc

20

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 57

tggaatggc tatgtcagtg

20

<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 58

ctggtaatct gtgtttagg

20

<210> 59

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 59

caagggcctc tccaaacttg

20

<210> 60

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 60

gccccagaga cagcattcca

20

<210> 61

<211> 268

<212> PRT

<213> Homo sapiens

<400> 61

Met Ala Gln Pro Leu Cys Pro Pro Leu Ser Glu Ser Trp Met Leu Ser

1

5

10

15

Ala Ala Trp Gly Pro Thr Arg Arg Pro Pro Pro Ser Asp Lys Asp Cys

20

25

30

Gly Arg Ser Leu Val Ser Ser Pro Asp Ser Trp Gly Ser Thr Pro Ala

35

40

45

Asp Ser Pro Val Ala Ser Pro Ala Arg Pro Gly Thr Leu Arg Asp Pro
50 55 60

Arg Ala Pro Ser Val Gly Arg Arg Gly Ala Arg Ser Ser Arg Leu Gly
65 70 75 80

Ser Gly Gln Arg Gln Ser Ala Ser Glu Arg Glu Lys Leu Arg Met Arg
85 90 95

Thr Leu Ala Arg Ala Leu His Glu Leu Arg Arg Phe Leu Pro Pro Ser
100 105 110

Val Ala Pro Ala Gly Gln Ser Leu Thr Lys Ile Glu Thr Leu Arg Leu
115 120 125

Ala Ile Arg Tyr Ile Gly His Leu Ser Ala Val Leu Gly Leu Ser Glu
130 135 140

Glu Ser Leu Gln Arg Arg Cys Arg Gln Arg Gly Asp Ala Gly Ser Pro
145 150 155 160

Arg Gly Cys Pro Leu Cys Pro Asp Asp Cys Pro Ala Gln Met Gln Thr
165 170 175

Arg Thr Gln Ala Glu Gly Gln Gly Gln Gly Arg Gly Leu Gly Leu Val
180 185 190

Ser Ala Val Arg Ala Gly Ala Ser Trp Gly Ser Pro Pro Ala Cys Pro
195 200 205

Gly Ala Arg Ala Ala Pro Glu Pro Arg Asp Pro Pro Ala Leu Phe Ala
210 215 220

Glu Ala Ala Cys Pro Glu Gly Gln Ala Met Glu Pro Ser Pro Pro Ser
225 230 235 240

acg ctg gcc cgc gcc ctg cac gag ctg cgc cgc ttt cta ccg ccg tcc 336
 Thr Leu Ala Arg Ala Leu His Glu Leu Arg Arg Phe Leu Pro Pro Ser
 100 105 110

gtg gcg ccc gcg ggc cag agc ctg acc aag atc gag acg ctg cgc ctg 384
 Val Ala Pro Ala Gly Gln Ser Leu Thr Lys Ile Glu Thr Leu Arg Leu
 115 120 125

gct atc cgc tat atc ggc cac ctg tcg gcc gtg cta ggc ctc agc gag 432
 Ala Ile Arg Tyr Ile Gly His Leu Ser Ala Val Leu Gly Leu Ser Glu
 130 135 140

gag agt ctc cag cgc cgg tgc cgg cag cgc ggt gac gcg ggg tcc cct 480
 Glu Ser Leu Gln Arg Arg Cys Arg Gln Arg Gly Asp Ala Gly Ser Pro
 145 150 155 160

cgg ggc tgc ccg ctg tgc ccc gac gac tgc ccc gcg cag atg cag aca 528
 Arg Gly Cys Pro Leu Cys Pro Asp Asp Cys Pro Ala Gln Met Gln Thr
 165 170 175

cgg acg cag gct gag ggg cag ggg cag ggg cgc ggg ctg ggc ctg gta 576
 Arg Thr Gln Ala Glu Gly Gln Gly Gln Gly Arg Gly Leu Gly Leu Val
 180 185 190

tcc gcc gtc cgc gcc ggg gcg tcc tgg gga tcc ccg cct gcc tgc ccc 624
 Ser Ala Val Arg Ala Gly Ala Ser Trp Gly Ser Pro Pro Ala Cys Pro
 195 200 205

gga gcc cga gct gca ccc gag ccg cgc gac ccg cct gcg ctg ttc gcc 672
 Gly Ala Arg Ala Ala Pro Glu Pro Arg Asp Pro Pro Ala Leu Phe Ala
 210 215 220

gag gcg gcg tgc cct gaa ggg cag gcg atg gag cca agc cca ccg tcc 720
 Glu Ala Ala Cys Pro Glu Gly Gln Ala Met Glu Pro Ser Pro Pro Ser
 225 230 235 240

cgc ctc ctt ccg ggc gac gtg ctg gct ctg ttg gag acc tgg atg ccc 768
 Pro Leu Leu Pro Gly Asp Val Leu Ala Leu Leu Glu Thr Trp Met Pro
 245 250 255

ctc tgc cct ctg gag tgg ctg cct gag gag ccc aag 804
 Leu Ser Pro Leu Glu Trp Leu Pro Glu Glu Pro Lys.
 260 265

<210> 63

<211> 215

<212> PRT

<213> Homo sapiens

<400> 63

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
 1 5 10 15

Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
 20 25 30

Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
 35 40 45

Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
 50 55 60

Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
 65 70 75 80

Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg
 85 90 95

Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys
 100 105 110

Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val
 115 120 125

Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala
 130 135 140

Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg
 145 150 155 160

Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys
 165 170 175

Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
 180 185 190

Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
 195 200 205

Thr Trp Ala Pro Glu Pro Arg
 210

<210> 64

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(648)

<400> 64

atg ggc agc ccc cgc tcc gcg ctg agc tgc ctg ctg ttg cac ttg ctg 48
 Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
 1 5 10 15

gtc ctc tgc ctc caa gcc cag gta act gtt cag tcc tca cct aat ttt 96
 Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
 20 25 30

aca cag cat gtg agg gag cag agc ctg gtg acg gat cag ctc agc cgc 144

Thr	Gln	His	Val	Arg	Glu	Gln	Ser	Leu	Val	Thr	Asp	Gln	Leu	Ser	Arg	
		35					40					45				
cgc	ctc	atc	cgg	acc	tac	caa	ctc	tac	agc	cgc	acc	agc	ggg	aag	cac	192
Arg	Leu	Ile	Arg	Thr	Tyr	Gln	Leu	Tyr	Ser	Arg	Thr	Ser	Gly	Lys	His	
	50					55					60					
gtg	cag	gtc	ctg	gcc	aac	aag	cgc	atc	aac	gcc	atg	gca	gag	gac	ggc	240
Val	Gln	Val	Leu	Ala	Asn	Lys	Arg	Ile	Asn	Ala	Met	Ala	Glu	Asp	Gly	
	65				70				75					80		
gac	ccc	ttc	gca	aag	ctc	atc	gtg	gag	acg	gac	acc	ttt	gga	agc	aga	288
Asp	Pro	Phe	Ala	Lys	Leu	Ile	Val	Glu	Thr	Asp	Thr	Phe	Gly	Ser	Arg	
				85					90					95		
gtt	cga	gtc	cga	gga	gcc	gag	acg	ggc	ctc	tac	atc	tgc	atg	aac	aag	336
Val	Arg	Val	Arg	Gly	Ala	Glu	Thr	Gly	Leu	Tyr	Ile	Cys	Met	Asn	Lys	
			100					105						110		
aag	ggg	aag	ctg	atc	gcc	aag	agc	aac	ggc	aaa	ggc	aag	gac	tgc	gtc	384
Lys	Gly	Lys	Leu	Ile	Ala	Lys	Ser	Asn	Gly	Lys	Gly	Lys	Asp	Cys	Val	
	115						120						125			
ttc	acg	gag	att	gtg	ctg	gag	aac	aac	tac	aca	gcg	ctg	cag	aat	gcc	432
Phe	Thr	Glu	Ile	Val	Leu	Glu	Asn	Asn	Tyr	Thr	Ala	Leu	Gln	Asn	Ala	
	130					135					140					
aag	tac	gag	ggc	tgg	tac	atg	gcc	ttc	acc	cgc	aag	ggc	cgg	ccc	cgc	480
Lys	Tyr	Glu	Gly	Trp	Tyr	Met	Ala	Phe	Thr	Arg	Lys	Gly	Arg	Pro	Arg	
	145				150					155				160		
aag	ggc	tcc	aag	acg	cgg	cag	cac	cag	cgt	gag	gtc	cac	ttc	atg	aag	528
Lys	Gly	Ser	Lys	Thr	Arg	Gln	His	Gln	Arg	Glu	Val	His	Phe	Met	Lys	
			165					170					175			
cgg	ctg	ccc	cgg	ggc	cac	cac	acc	acc	gag	cag	agc	ctg	cgc	ttc	gag	576

Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
 180 185 190

ttc ctc aac tac ccg ccc ttc acg cgc agc ctg cgc ggc agc cag agg 624
 Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
 195 200 205

act tgg gcc ccg gaa ccc cga 645
 Thr Trp Ala Pro Glu Pro Arg
 210 215

<210> 65

<211> 212

<212> PRT

<213> Homo sapiens

<400> 65

Met Asp Tyr Leu Leu Met Ile Phe Ser Leu Leu Phe Val Ala Cys Gln
 1 5 10 15

Gly Ala Pro Glu Thr Ala Val Leu Gly Ala Glu Leu Ser Ala Val Gly
 20 25 30

Glu Asn Gly Gly Glu Lys Pro Thr Pro Ser Pro Pro Trp Arg Leu Arg
 35 40 45

Arg Ser Lys Arg Cys Ser Cys Ser Ser Leu Met Asp Lys Glu Cys Val
 50 55 60

Tyr Phe Cys His Leu Asp Ile Ile Trp Val Asn Thr Pro Glu His Val
 65 70 75 80

Val Pro Tyr Gly Leu Gly Ser Pro Arg Ser Lys Arg Ala Leu Glu Asn
 85 90 95

Leu Leu Pro Thr Lys Ala Thr Asp Arg Glu Asn Arg Cys Gln Cys Ala
 100 105 110

Ser Gln Lys Asp Lys Lys Cys Trp Asn Phe Cys Gln Ala Gly Lys Glu
 115 120 125

Leu Arg Ala Glu Asp Ile Met Glu Lys Asp Trp Asn Asn His Lys Lys
 130 135 140

Gly Lys Asp Cys Ser Lys Leu Gly Lys Lys Cys Ile Tyr Gln Gln Leu
 145 150 155 160

Val Arg Gly Arg Lys Ile Arg Arg Ser Ser Glu Glu His Leu Arg Gln
 165 170 175

Thr Arg Ser Glu Thr Met Arg Asn Ser Val Lys Ser Ser Phe His Asp
 180 185 190

Pro Lys Leu Lys Gly Lys Pro Ser Arg Glu Arg Tyr Val Thr His Asn
 195 200 205

Arg Ala His Trp
 210

<210> 66

<211> 636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(639)

<400> 66

atg gat tat ttg ctc atg att ttc tct ctg ctg ttt gtg gct tgc caa 48
 Met Asp Tyr Leu Leu Met Ile Phe Ser Leu Leu Phe Val Ala Cys Gln
 1 5 10 15

gga gct cca gaa aca gca gtc tta ggc gct gag ctc agc gcg gtg ggt 96
 Gly Ala Pro Glu Thr Ala Val Leu Gly Ala Glu Leu Ser Ala Val Gly
 20 25 30

gag aac ggc ggg gag aaa ccc act ccc agt cca ccc tgg cgg ctc cgc 144
 Glu Asn Gly Gly Glu Lys Pro Thr Pro Ser Pro Pro Trp Arg Leu Arg
 35 40 45

cgg tcc aag cgc tgc tcc tgc tgc tcc ctg atg gat aaa gag tgt gtc 192
 Arg Ser Lys Arg Cys Ser Cys Ser Ser Leu Met Asp Lys Glu Cys Val
 50 55 60

tac ttc tgc cac ctg gac atc att tgg gtc aac act ccc gag cac gtt 240
 Tyr Phe Cys His Leu Asp Ile Ile Trp Val Asn Thr Pro Glu His Val
 65 70 75 80

gtt cgg tat gga ctt gga agc cct agg tcc aag aga gcc ttg gag aat 288
 Val Pro Tyr Gly Leu Gly Ser Pro Arg Ser Lys Arg Ala Leu Glu Asn
 85 90 95

tta ctt ccc aca aag gca aca gac cgt gag aat aga tgc caa tgt gct 336
 Leu Leu Pro Thr Lys Ala Thr Asp Arg Glu Asn Arg Cys Gln Cys Ala
 100 105 110

agc caa aaa gac aag aag tgc tgg aat ttt tgc caa gca gga aaa gaa 384
 Ser Gln Lys Asp Lys Lys Cys Trp Asn Phe Cys Gln Ala Gly Lys Glu
 115 120 125

ctc agg gct gaa gac att atg gag aaa gac tgg aat aat cat aag aaa 432
 Leu Arg Ala Glu Asp Ile Met Glu Lys Asp Trp Asn Asn His Lys Lys
 130 135 140

gga aaa gac tgt tcc aag ctt ggg aaa aag tgt att tat cag cag tta 480
 Gly Lys Asp Cys Ser Lys Leu Gly Lys Lys Cys Ile Tyr Gln Gln Leu
 145 150 155 160

gtg aga gga aga aaa atc aga aga agt tca gag gaa cac cta aga caa 528
 Val Arg Gly Arg Lys Ile Arg Arg Ser Ser Glu Glu His Leu Arg Gln
 165 170 175

acc agg tcg gag acc atg aga aac agc gtc aaa tca tct ttt cat gat 576
 Thr Arg Ser Glu Thr Met Arg Asn Ser Val Lys Ser Ser Phe His Asp
 180 185 190

ccc aag ctg aaa ggc aag ccc tcc aga gag cgt tat gtg acc cac aac 624
 Pro Lys Leu Lys Gly Lys Pro Ser Arg Glu Arg Tyr Val Thr His Asn
 195 200 205

cga gca cat tgg 636
 Arg Ala His Trp
 210

<210> 67

<211> 143

<212> PRT

<213> Homo sapiens

<400> 67

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
 1 5 10 15

Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
 20 25 30

Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
 35 40 45

Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
 50 55 60

Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
 65 70 75 80

Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly
 85 90 95

Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
 100 105 110

Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
 115 120 125

Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
 130 135 140

<210> 68

<211> 429

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(432)

<400> 68

atg cag cac cga ggc ttc ctc ctc ctc acc ctc ctc gcc ctg ctg gcg 48
 Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
 1 5 10 15

ctc acc tcc gcg gtc gcc aaa aag aaa gat aag gtg aag aag gcc gcc 96
 Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
 20 25 30

ccg ggg agc gag tgc gct gag tgg gcc tgg ggg ccc tgc acc ccc agc 144
 Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
 35 40 45

agc aag gat tgc gcc gtg ggt ttc cgc gag gcc acc tgc ggg gcc cag 192
 Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
 50 55 60

acc cag cgc atc cgg tgc agg gtg ccc tgc aac tgg aag aag gag ttt 240
 Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
 65 70 75 80

gga gcc gac tgc aag tac aag ttt gag aac tgg ggt gcg tgt gat ggg 288
 Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly

85

90

95

ggc aca ggc acc aaa gtc cgc caa ggc acc ctg aag aag gcg cgc tac 336
 Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
 100 105 110

aat gct cag tgc cag gag acc atc cgc gtc acc aag ccc tgc acc ccc 384
 Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
 115 120 125

aag acc aaa gca aag gcc aaa gcc aag aaa ggg aag gga aag gac 429
 Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
 130 135 140

<210> 69

<211> 408

<212> PRT

<213> Homo sapiens

<400> 69

Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val
 1 5 10 15

Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys
 20 25 30

Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly
 35 40 45

Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
 50 55 60

Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
 65 70 75 80

Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu
 85 90 95

Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
100 105 110

Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
115 120 125

Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
130 135 140

Ser Ser Ile Pro Glu Asn Glu Ala Ile Ser Ser Ala Glu Leu Arg Leu
145 150 155 160

Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His
165 170 175

Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro
180 185 190

Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn
195 200 205

Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp
210 215 220

Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
225 230 235 240

Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
245 250 255

Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
260 265 270

Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
275 280 285

Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
 290 295 300

Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
 305 310 315 320

Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
 325 330 335

Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
 340 345 350

Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
 355 360 365

Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
 370 375 380

Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
 385 390 395 400

Val Val Glu Gly Cys Gly Cys Arg
 405

<210> 70

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1227)

<400> 70

atg att cct ggt aac cga atg ctg atg gtc gtt tta tta tgc caa gtc 48

Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val

1

5

10

15

ctg cta gga ggc gcg agc cat gct agt ttg ata cct gag acg ggg aag 96

Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys
 20 25 30

aaa aaa gtc gcc gag att cag ggc cac gcg gga gga cgc cgc tca ggg 144
 Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly
 35 40 45

cag agc cat gag ctc ctg cgg gac ttc gag gcg aca ctt ctg cag atg 192
 Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
 50 55 60

ttt ggg ctg cgc cgc cgc ccg cag cct agc aag agt gcc gtc att ccg 240
 Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
 65 70 75 80

gac tac atg cgg gat ctt tac cgg ctt cag tct ggg gag gag gag gaa 288
 Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu
 85 90 95

gag cag atc cac agc act ggt ctt gag tat cct gag cgc ccg gcc agc 336
 Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
 100 105 110

cgg gcc aac ace gtg agg agc ttc cac cac gaa gaa cat ctg gag aac 384
 Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
 115 120 125

atc cca ggg acc agt gaa aac tct get ttt cgt ttc ctc ttt aac ctc 432
 Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
 130 135 140

agc agc atc cct gag aac gag gcg atc tcc tct gca gag ctt cgg ctc 480
 Ser Ser Ile Pro Glu Asn Glu Ala Ile Ser Ser Ala Glu Leu Arg Leu
 145 150 155 160

ttc cgg gag cag gtg gac cag ggc cct gat tgg gaa agg ggc ttc cac 528

Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His	
165	170 175
cgt ata aac att tat gag gtt atg aag ccc cca gca gaa gtg gtg cct	576
Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro	
180	185 190
ggg cac ctc atc aca cga cta ctg gac acg aga ctg gtc cac cac aat	624
Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn	
195	200 205
gtg aca cgg tgg gaa act ttt gat gtg agc cct gcg gtc ctt cgc tgg	672
Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp	
210	215 220
acc cgg gag aag cag cca aac tat ggg cta gcc att gag gtg act cac	720
Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His	
225	230 235 240
ctc cat cag act cgg acc cac cag ggc cag cat gtc agg att agc cga	768
Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg	
245	250 255
tcg tta cct caa ggg agt ggg aat tgg gcc cag ctc cgg ccc ctc ctg	816
Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu	
260	265 270
gtc acc ttt ggc cat gat ggc cgg ggc cat gcc ttg acc cga cgc cgg	864
Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg	
275	280 285
agg gcc aag cgt agc cct aag cat cac tca cag cgg gcc agg aag aag	912
Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys	
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